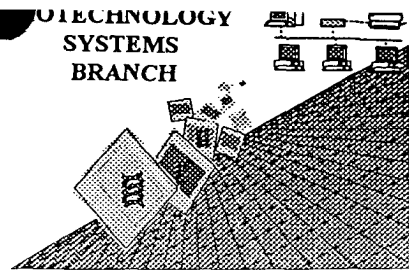# CRF Diskette Problem Report

The Scientific and Technical Information Center (STIC) experienced a problem when processing the following CRF diskette:

Application Serial Number: _08/779,460A_

Filing Date: _1/7/97_

Classification: _800_

Date Processed by STIC: _10/27/97_

Point-of-Contact/Telephone No.: **Arti Shah   703 - 308 - 4212**

Nature of Problem:

The diskette was:

__ Damaged

__ Unreadable

__ Blank (no files present on diskette)

__ Contained an empty file (filename present, but no bytes in file)

__ A computer virus was detected on the diskette. The STIC will not process the diskette through the Data Capture System.

   Name of virus: _____

✓ The Sequence Listing was not saved in ASCII (DOS) text.

__ The diskette contained an error that disrupted normal processing:

_____
_____
_____

AGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION   *US/08/779,460B*

DATE: 04/09/98
TIME: 13:14:18

INPUT SET: S24825.raw

> **This Raw Listing c ntains the General**
> **Information Section and up to the first 5 pages.**

```
                                      SEQUENCE LISTING

     (1)    General Information:                        Does Not Comply
                                               Corrected Diskette Needed
-->        (i)  APPLICANTS:

                Oscar Johannes Maria GODDIJN
                Teunis Cornelis VERWOERD
                Ronny Wilhelmus Hermanus Henrika KRUTWAGEN
                Eline VOOGD

-->        (ii) TITLE OF INVENTION:

                ENHANCED ACCUMULATION OF TREHALOSE IN PLANTS

           (iii)    NUMBER OF SEQUENCES: 27

           (iv) CORRESPONDENCE ADDRESS:

                (A)  ADDRESSEE:              LADAS & PARRY

                (B)  STREET:         26 WEST 61 STREET

                (C)  CITY:                  NEW YORK

                (D)  STATE:          NY

                (F)(B) ZIP:          10023

                (E)(F) COUNTRY:      USA

           (v)  COMPUTER READABLE FORM:

                (A)  MEDIUM TYPE:    3-1/4" Disk    1.44 MB

                (B)  COMPUTER:       IBM PC Compatible

                (C)  OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11

                (D)  SOFTWARE:       WordPerfect 6.1 for Windows

           (vi) CURRENT APPLICATION DATA:

                (A)  APPLICATION NUMBER:      08/779,460

                (B)  FILING DATE:    07-JAN-1997
```

```
47
48       (C)   CLASSIFICATION:          435
49
50
51    (vii)    PRIOR APPLICATION DATA:
52
53       (A)   APPLICATION NUMBER:      PY000009/96
54
55       (B)   FILING DATE:     12-JAN-1996
56
57    (viii)   ATTORNEY/AGENT INFORMATION:
58
59       (A)   NAME:                    MASS, Clifford J.
60
61       (B)   REGISTRATION NO.: 30,086
62
63       (C)   REF./DOCKET NO.:  U-011098-6
64
65    (ix) TELECOMMUNICATION INFORMATION:
66
67       (A)   TELEPHONE NUMBER: (212) 708-1890
68                 TELEFAX
69       (B)   TELEAX NUMBER:           (212)- 246-8959
70
71       (C)   TELEX NUMBER:            233288
72
73
74  (2) INFORMATION FOR SEQ ID NO: 1:
75
76     (i) SEQUENCE CHARACTERISTICS:
77             (A) LENGTH: 2621 base pairs
78             (B) TYPE: nucleic acid
79             (C) STRANDEDNESS: double
80             (D) TOPOLOGY: linear
81
82     (ii) MOLECULE TYPE: cDNA to mRNA
83
84     (iii) HYPOTHETICAL: NO
85
86     (ix) FEATURE:
87             (A) NAME/KEY: CDS
88             (B) LOCATION: 25..2485
89             (D) OTHER INFORMATION: /function= "trehalose phosph.
90                     synthase and trehalose phosph. phosphatase"
91                     /product= "bipartite enzyme"
92
93     (ix) FEATURE:
94             (A) NAME/KEY: unsure
95             (B) LOCATION: 1609..1611
96
97
98     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
99
```

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/779,460B

INPUT SET: S24825.raw

```
100   CTGATCCTGC GGTTTCATCA CAAT ATG ATA CTC TTA CAT CTG ATG CCC CTT        51
101                              Met Ile Leu Leu His Leu Met Pro Leu
102                               1                   5

103
104   CAG ATG CTC CCA AAT AGG TTG ATT GTC GTA TCG AAT CAG TTA CCC ATA        99
105   Gln Met Leu Pro Asn Arg Leu Ile Val Val Ser Asn Gln Leu Pro Ile
106    10              15                  20                  25

107
108   ATC GCT AGG CTA AGA CTA ACG ACA ATG GAG GGT CCT TTT GGG ATT TCA       147
109   Ile Ala Arg Leu Arg Leu Thr Thr Met Glu Gly Pro Phe Gly Ile Ser
110                30                  35                  40

111
112   CTT GGG ACG AGA GTT CGA TTT ACA TGC ACA TCA AAG ATG CAT TAC CCG       195
113   Leu Gly Thr Arg Val Arg Phe Thr Cys Thr Ser Lys Met His Tyr Pro
114                45                  50                  55

115
116   CAG CCG TTG AGG TTT TCT ATT CTT GGC GAT CCA CTA AGG GCT GAC GTT       243
117   Gln Pro Leu Arg Phe Ser Ile Leu Gly Asp Pro Leu Arg Ala Asp Val
118                60                  65                  70

119
120   GGC CCT ACC GAA CAA GAT GAC GTG TCA AAG ACA TTG CTC GAT AGG TTT       291
121   Gly Pro Thr Glu Gln Asp Asp Val Ser Lys Thr Leu Leu Asp Arg Phe
122        75                  80                  85

123
124   AAT TGC GTT GCG GTT TTT GTC CCT ACT TCA AAA TGG GAC CAA TAT TAT       339
125   Asn Cys Val Ala Val Phe Val Pro Thr Ser Lys Trp Asp Gln Tyr Tyr
126    90              95                  100                 105

127
128   CAC TGC TTT TGT AAG CAG TAT TTG TGG CCG ATA TTT CAT TAC AAG GTT       387
129   His Cys Phe Cys Lys Gln Tyr Leu Trp Pro Ile Phe His Tyr Lys Val
130                110                 115                 120

131
132   CCC GCT TCT GAC GTC AAG AGT GTC CCG AAT AGT CGG GAT TCA TGG AAC       435
133   Pro Ala Ser Asp Val Lys Ser Val Pro Asn Ser Arg Asp Ser Trp Asn
134                125                 130                 135

135
136   GCT TAT GTT CAC GTG AAC AAA GAG TTT TCC CAG AAG GTG ATG GAG GCA       483
137   Ala Tyr Val His Val Asn Lys Glu Phe Ser Gln Lys Val Met Glu Ala
138                140                 145                 150

139
140   GTA ACC AAT CGT AGC AAT TAT GTA TGG ATA CAT GAC TAC CAT TTA ATG       531
141   Val Thr Asn Arg Ser Asn Tyr Val Trp Ile His Asp Tyr His Leu Met
142        155                 160                 165

143
144   ACG CTA CCG ACT TTC TTG AGG CGG GAT TTT TGT CGT TTT AAA ATC GGT       579
145   Thr Leu Pro Thr Phe Leu Arg Arg Asp Phe Cys Arg Phe Lys Ile Gly
146   170                 175                 180                 185

147
148   TTT TTT CTG CAT AGC CCG TTT CCT TCC TCG GAG GTT TAC AAG ACC CTA       627
149   Phe Phe Leu His Ser Pro Phe Pro Ser Ser Glu Val Tyr Lys Thr Leu
150                190                 195                 200

151
152   CCA ATG AGA AAC GAG CTC TTG AAG GGT CTG TTA AAT GCT GAT CTT ATC       675
```

INPUT SET: S24825.raw

```
153   Pro Met Arg Asn Glu Leu Leu Lys Gly Leu Leu Asn Ala Asp Leu Ile
154           205                   210               215
155
156   GGG TTC CAT ACA TAC GAT TAT GCC CGT CAT TTT CTA ACG TGT TGT AGT      723
157   Gly Phe His Thr Tyr Asp Tyr Ala Arg His Phe Leu Thr Cys Cys Ser
158           220                   225               230
159
160   CGA ATG TTT GGT TTG GAT CAT CAG TTG AAA AGG GGG TAC ATT TTC TTG      771
161   Arg Met Phe Gly Leu Asp His Gln Leu Lys Arg Gly Tyr Ile Phe Leu
162           235                   240               245
163
164   GAA TAT AAT GGA AGG AGC ATT GAG ATC AAG ATA AAG GCG AGC GGG ATT      819
165   Glu Tyr Asn Gly Arg Ser Ile Glu Ile Lys Ile Lys Ala Ser Gly Ile
166   250                   255               260                   265
167
168   CAT GTT GGT CGA ATG GAG TCG TAC TTG AGT CAG CCC GAT ACA AGA TTA      867
169   His Val Gly Arg Met Glu Ser Tyr Leu Ser Gln Pro Asp Thr Arg Leu
170                   270               275               280
171
172   CAA GTT CAA GAA GTC CAA AAA CGT TCG AAG GAA ATC GTG CTA CTG GGA      915
173   Gln Val Gln Glu Val Gln Lys Arg Ser Lys Glu Ile Val Leu Leu Gly
174           285                   290               295
175
176   GTT GAT GAT TTG GAT ATA TTC AAA GGT GTG AAC TTC AAG GTT TTA GCG      963
177   Val Asp Asp Leu Asp Ile Phe Lys Gly Val Asn Phe Lys Val Leu Ala
178           300                   305               310
179
180   TTG GAG AAG TTA CTT AAA TCA CAC CCG AGT TGG CAA GGG CGT GTG GAA     1011
181   Leu Glu Lys Leu Leu Lys Ser His Pro Ser Trp Gln Gly Arg Val Glu
182           315                   320               325
183
184   AAG GTG CAA ATC TTG AAT CCT CTG CGC CGT TGC CAA GAC GTC GAT GAG     1059
185   Lys Val Gln Ile Leu Asn Pro Leu Arg Arg Cys Gln Asp Val Asp Glu
186   330                   335               340                   345
187
188   ATC AAT GCC GAG ATA AGA ACA GTC TGT GAA AGA ATC AAT AAC GAA CTG     1107
189   Ile Asn Ala Glu Ile Arg Thr Val Cys Glu Arg Ile Asn Asn Glu Leu
190                   350               355               360
191
192   GGA AGC CCG GGA TAC CAG CCC GTT GTG TTA ATT GAT GGG CCC GTT TCG     1155
193   Gly Ser Pro Gly Tyr Gln Pro Val Val Leu Ile Asp Gly Pro Val Ser
194                   365               370               375
195
196   TTA AGT GAA AAA GCT GCT TAT TAT GCT ATC GCC GAT ATG GCA ATT GTT     1203
197   Leu Ser Glu Lys Ala Ala Tyr Tyr Ala Ile Ala Asp Met Ala Ile Val
198           380                   385               390
199
200   ACA CCG TTA CGT GAC GGA CTG AAT CTT ATC CCG TAC GAG TAC GTC GTT     1251
201   Thr Pro Leu Arg Asp Gly Leu Asn Leu Ile Pro Tyr Glu Tyr Val Val
202           395                   400               405
203
204   TCC CGA CAA AGT GTT AAT GAC CCA AAT CCC AAT ACT CCA AAA AAG AGC     1299
205   Ser Arg Gln Ser Val Asn Asp Pro Asn Pro Asn Thr Pro Lys Lys Ser
```

INPUT SET: S24825.raw

```
206   410                      415                    420                     425
207
208   ATG CTA GTG GTC TCC GAG TTC ATC GGT GTT TCA CTA TCT TTA ACC GGG        1347
209   Met Leu Val Val Ser Glu Phe Il  Gly Val Ser Leu Ser Leu Thr Gly
210                    430                  435                  440
211
212   GCC ATA CGG GTC AAC CCA TGG GAT GAG TTG GAG ACA GCA GAA GCA TTA        1395
213   Ala Ile Arg Val Asn Pro Trp Asp Glu Leu Glu Thr Ala Glu Ala Leu
214                    445                  450                  455
215
216   TAC GAC GCA CTC ATG GCT CCT GAT GAC CAT AAA GAA ACC GCC CAC ATG        1443
217   Tyr Asp Ala Leu Met Ala Pro Asp Asp His Lys Glu Thr Ala His Met
218                    460                  465                  470
219
220   AAA CAG TAT CAA TAC ATT ATC TCC CAT GAT GTA GCT AAC TGG GCT AGC        1491
221   Lys Gln Tyr Gln Tyr Ile Ile Ser His Asp Val Ala Asn Trp Ala Ser
222        475                  480                  485
223
224   TTC TTT CAA GAT TTA GAG CAA GCG TGC ATC GAT CAT TCT CGT AAA CGA        1539
225   Phe Phe Gln Asp Leu Glu Gln Ala Cys Ile Asp His Ser Arg Lys Arg
226   490                  495                  500                  505
227
228   TGC ATG AAT TTA GGA TTT GGG TTA GAT ACT AGA GTC GTC TTT TTG ATG        1587
229   Cys Met Asn Leu Gly Phe Gly Leu Asp Thr Arg Val Val Phe Leu Met
230                    510                  515                  520
231
232   AGA AGT TTA GCA AGT TGG ATA AAG ATG TCT TGG AAG AAT GCT TAT TCC        1635
233   Arg Ser Leu Ala Ser Trp Ile Lys Met Ser Trp Lys Asn Ala Tyr Ser
234                    525                  530                  535
235
236   ATG GCT CAA AAT CGG GCC ATA CTT TTG GAC TAT GAC GGC ACT GTT ACT        1683
237   Met Ala Gln Asn Arg Ala Ile Leu Leu Asp Tyr Asp Gly Thr Val Thr
238                    540                  545                  550
239
240   CCA TCT ATC AGT AAA TCT CCA ACT GAA GCT GTT ATC TCC ATG ATC AAC        1731
241   Pro Ser Ile Ser Lys Ser Pro Thr Glu Ala Val Ile Ser Met Ile Asn
242        555                  560                  565
243
244   AAA CTG TGC AAT GAT CCA AAG AAC ATG GTG TTC ATC GTT AGT GGA CGC        1779
245   Lys Leu Cys Asn Asp Pro Lys Asn Met Val Phe Ile Val Ser Gly Arg
246   570                  575                  580                  585
247
248   AGT AGA GAG AAA ATC TTG GCA GTT GGT TCG GCG CGT GTG AGA ACC CGC        1827
249   Ser Arg Glu Lys Ile Leu Ala Val Gly Ser Ala Arg Val Arg Thr Arg
250                    590                  595                  600
251
252   CAT TGC ACT GAG CAC GGA TAC TTT ATA AGG TGG GCG GGT GAT CAA GAA        1875
253   His Cys Thr Glu His Gly Tyr Phe Ile Arg Trp Ala Gly Asp Gln Glu
254                    605                  610                  615
255
256   TGG GAA ACG TGC GCA CGT GAG AAT AAT GTC GGG TGG ATG GAT GGA AAT        1923
257   Trp Glu Thr Cys Ala Arg Glu Asn Asn Val Gly Trp Met Asp Gly Asn
258                    620                  625                  630
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/779,460B*

e	Error	Original Text
	Mandatory Value Not Present	(i) APPLICANTS:
	Mandatory Value Not Present	(ii) TITLE OF INVENTION:
	Wrong Classification	(C) CLASSIFICATION: 435
	Unknown or Misplaced Identifier	(B) TELEAX NUMBER: (212)- 246-8959